Amendments to the Claims:

1. (currently amended) A method for the identification of suitable fragmentation sites in a reporter protein, wherein the reporter protein is detectable when active, the method comprising the steps of:

(a) providing a DNA sequence encoding for said reporter protein ;

(b) creating a library based on the DNA sequence as defined in (a),

- wherein each individual of said library comprises a randomly created first subsequence of the DNA sequence as defined in (a), encoding for a first subdomain of said reporter protein, and
- wherein each individual of said library comprises a randomly created complementary second subsequence of the DNA sequence as defined in (a), encoding for a complementary second subdomain of said reporter protein;

(c) screening ~~and/or selection~~ for restoration of detectable activity of said reporter protein, when said first subdomain and said complementary second subdomain are brought into close spatial proximity so as to allow reconstitution of both first and second subdomains into an active protein comprising steps of

- creating a first fusion subsequence comprising the first subsequence of said reporter protein as defined in step (b), fused to an oligonucleotide encouding for a first protein or peptide and
- creating a second fusion subsequence comprising the complementary second subsequence of said reporter protein as defined in (b), fused to an oligonucleotide encoding for a second protein or peptide,

wherein said first and said second protein or peptide are known to interact; and

(d) identifying said first subdomain and/or said first subsequence, and said complementary second subdomain and/or said complementary second subsequence, that lead to restoration of detectable activity of said reporter protein.

2. (Original) A method according to claim 1, wherein the reporter protein is detectable in vivo and/or in vitro, both as full length protein and when actively resembled by a first subdomain and a complementary second subdomain, by a means chosen from the group consisting of color assays and growth assays.

3. (currently amended) A method according to claim 1, wherein individuals of the library as defined in (b) are either prokaryotic or eukaryotic host cells, comprising:

- both said first subsequence and said complementary second subsequence in one ~~and the same~~ expression vector, suitable for (co-) expression of said first subsequence and said complementary second subsequence in vivo ; or
- said first subsequence in a first expression vector suitable for (co-) expression of said first subsequence, and said complementary second subsequence in a second expression vector suitable for (co-) expression of said complementary second subsequence.

4. (previously presented) A method according to claim 1, wherein screening for restoration of detectable activity of said reporter protein, when said first subdomain and said complementary second subdomain are brought into close proximity as defined in (c), comprises the following steps:

- creating a first fusion subsequence comprising the first subsequence of said reporter protein as defined in (b), fused to an oligonucleotide encoding for a first protein or peptide,
- creating a second fusion subsequence comprising the complementary second subsequence of said reporter protein as defined in (b), fused to an oligonucleotide encoding for a second protein or peptide, wherein said first protein or peptide and said second protein or peptide are known to interact.

5. (currently amended) A method according to claim [[4]] 1, wherein said first protein or peptide and said second protein or peptide align to each other in an anti-parallel coiled coil orientation.

6. (Original) A method according to claim 5, wherein said first protein or peptide and said second protein or peptide are leucine zippers.

7. (previously presented) A method according to claim 4, wherein said first fusion subsequence and said second subsequence are created by blunt end ligation.

8. (currently amended) A method according to claim 7, wherein said first fusion subsequence and said second fusion subsequence each comprise

- a linker sequence in between said first subsequence (or said second subsequence, respectively) and said oligonucleotide encoding for a first protein or peptide (or said oligonucleotide encoding for a second protein or peptide, respectively) ;
- at least one tag that allows for verification of the transcription of said first fusion subsequence and said second fusion subsequence into a polypeptide.

9. (previously presented) A method according to claim 4, wherein an oligonucleotide is inserted by homologous recombination in between said first subsequence and said second subsequence, encoding for:

- a transcription terminating sequence for terminating transcription of said first or said second subsequence;
- a transcription promoting sequence for initiating transcription of said second or said first subsequence, respectively ;
- a marker sequence allowing for control of successful homologous recombination.

10. (currently amended) A method according to claim 1, comprising the steps of:

- creating fragmentation sites in TRP1 using gene cleavage with a unique restriction enzyme RE1 and circularization;
- isolating fragments corresponding to the wild-type length of TRP1;

- sub-cloning using blunt ends preferably into a pRS316 based yeast expression vector under the control of a copper promoter (pCUBl) and transforming into E. coli, preferably XLlblue ;
- recombining and amplifying homologues with a unique restriction site RE2, preferably AvrII, introduced between the original N-and C-termini of TRP-1 to allow subsequent linerization of the vector;
- locating two leucine zippers in the ~~plasmid~~ expression vector at the 3'-and the 5'-ends of the newly generated N-and Ctermini, the leucine zippers being positive and negative charged helices to allow heterodimerization, preferably each heterodimer containing a buried asparagine residue in a position to force antiparallel orientation of the leucine zippers.

11. (Original) A recombinant DNA sequence for use in securing expression in a prokaryotic or eukaryotic host cell of a polypeptide product having the primary structural conformation of a first subdomain of a reporter protein or a complementary second subdomain of a reporter protein, wherein detectable activity of said reporter protein is restored, when said first subdomain and said complementary second subdomain are brought into close proximity, and wherein said first and said complementary second subdomain are not subdomains of one of the group of proteins consisting of transcriptional activators, ubiquitin, dihydrofolate reductase, β-lactamase, green fluorescent protein, β-galactosidase, inteins, cAMP cyclase, glycinamide ribonucleotide transformylase, aminoglycoside phosphotransferase, hygromycin B phosphotransferase, luciferase.

12. (Original) A recombinant DNA sequence according to claim 11, wherein said DNA sequence encodes for a subdomain of a $(\beta/\alpha)_8$-barrel enzyme.

13. (currently amended) A recombinant DNA sequence according to claim ~~11y~~ 11, wherein said DNA sequence is selected from the group consisting of:

(a) the DNA sequences SEQ ID NO 3, 5, 7, 9, 11, 13, 15, 17 or their complementary strands;

(b) DNA sequences which hybridize under stringent conditions to the protein coding regions of the DNA sequences defined in (a) or fragments thereof;

(c) DNA sequences which, but for the degeneracy of the genetic code, would hybridize to the DNA sequences defined in (a) or (b) and which sequences code for a polypeptide having the same amino acid sequence.

14. (previously presented) A recombinant DNA sequence according to claim 11, wherein said DNA sequence is for use in securing expression in a prokaryotic or eukaryotic host cell of a polypeptide fusion product.

15. (Original) A first subdomain of a reporter protein and/or a complementary second subdomain of a reporter protein, wherein detectable activity of said reporter protein is restored, when said first subdomain and said complementary second subdomain are brought into close proximity, and wherein said first and said complementary second subdomain are not subdomains of one of the group of proteins consisting of transcriptional activators, ubiquitin, dihydrofolate reductase, β-lactamase, green fluorescent protein, β-galactosidase, inteins, cAMP cyclase, glycinamide ribonucleotide transformylase, aminoglycoside phosphotransferase, hygromycin B phosphotransferase, luciferase.

16. (previously presented) A first subdomain of a reporter protein or a complementary second subdomain of a reporter protein according to claim 15, wherein the site of fragmentation of said reporter protein into a first subdomain and a complementary second subdomain is identified by a method according to claim 1.

17. (previously presented) A first subdomain of a reporter protein or a complementary second subdomain of a reporter protein, produced by a method of culturing a host transformed with a recombinant DNA molecule selected from the group consisting of the DNA molecules of claim 11, wherein said molecules further comprises an expression control sequence, said expression control sequence being operatively linked to said molecule.

18. (previously presented) A fusion protein comprising a first subdomain of a reporter protein or a complementary second subdomain of a reporter protein according to claim 15, and a further peptide or protein connected thereto in a naturally not occurring combination.

19. (previously presented) A prokaryotic or eukaryotic host cell line, transformed with a recombinant DNA sequence according to claim 11.

20. (Original) A host cell line according to claim 19, wherein the host cell line allows for homologous recombination of DNA.

21. (Original) A host cell line according to claim 20, which host cell line comprises a yeast cell line.

22. (Original) A host cell line according to claim 21, which yeast cell line is chosen from the group consisting of *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe*.

23. (Original) A kit of parts, comprising a first and a second DNA-based expression vector, wherein

- said first expression vector contains an expression cassette encoding for a polypeptide product having at least a substantial part of the primary structural confirmation of a first subdomain of a reporter protein; and
- said second expression vector contains an expression cassette encoding for a polypeptide product having at least a substantial part of the primary structural confirmation of a complementary second subdomain of a reporter protein; and

wherein detectable activity of said reporter protein is restored, when said first subdomain and said complementary second subdomain are brought into close proximity, and wherein said first and said complementary second subdomain are not subdomains of one the group of proteins consisting of transcriptional activators, ubiquitin, dihydrofolate reductase, ß-lactamase, green fluorescent protein, β-galactosidase, inteins, cAMP cyclase, glycinamide ribonucleotide transformylase, aminoglycoside phosphotransferase, hygromycin B phosphotransferase, luciferase.

24. (Original) A kit of parts according to claim 23, further comprising a suitable prokaryotic or eukaryotic host cell line for expression of said first and second expression vector.

25. (previously presented) A method for detecting an interaction between a first test peptide or protein or a fragment thereof, and a second test peptide or protein or a fragment thereof, the method comprising the steps of:

- providing recombinant DNA sequences according to claim 11 for use in securing expression of a first subdomain of a reporter protein and a complementary second subdomain of a reporter protein;
- fusing an oligonucleotide or a gene encoding for a first test peptide or protein to the DNA sequence encoding for said first subdomain of the reporter protein, thereby creating a first DNA fusion sequence encoding for a fusion protein comprising said first subdomain of the reporter protein and said first test peptide or protein;
- fusing an oligonucleotide or a gene encoding for a second test peptide or protein to the DNA sequence encoding for said complementary second subdomain of the reporter protein, thereby creating a second DNA fusion sequence encoding for a fusion protein comprising said complementary second subdomain of the reporter protein and said second test peptide or protein;
- (co-) expressing said fusion protein comprising said first subdomain of the reporter protein and said first test peptide or protein, and said fusion protein comprising said second complementary subdomain of the reporter protein and said second test peptide or protein in a suitable prokaryotic or eukaryotic host cell;
- screening and/or selecting for restoration of detectable activity of said reporter protein.

26. (Original) A method according to claim 25, wherein a library of oligonucleotides or DNA encoding for a set of first test peptides or proteins and/or a library of oligonucleotides or DNA encoding for a set of second test peptides or proteins are fused to said first subdomain of said reporter protein and/or said complementary second subdomain of said reporter protein, respectively.

27. (previously presented) A method according to claim 25, wherein said first test peptide or protein or a fragment thereof, and said second test peptide or protein or a fragment thereof, are peptides or proteins naturally occurring in compartments chosen from the group consisting of cellular membranes, the cytosol, the mitochondrium, the peroxisome and the lumen of the secretory path.

28. (previously presented) A method according to claim 25, wherein said interaction between a first test peptide or protein or a fragment thereof and a second test peptide or protein or fragment thereof is mediated by a chemical inducer of dimerization, which binds either covalently or non-covalently to both said test peptides or proteins or fragments thereof.

29. (previously presented) A method for detecting the interruption of an interaction between a first test peptide or protein or a fragment thereof, and a second test peptide or protein or a fragment thereof, the method comprising the steps of:

- providing recombinant DNA sequences according to claim 11 for use in securing expression of a first subdomain of a reporter protein and a complementary second subdomain of a reporter protein;
- fusing an oligonucleotide or a gene encoding for a first test peptide or protein to the DNA sequence encoding for said first subdomain of the reporter protein, thereby creating a first DNA fusion sequence encoding for a fusion protein comprising said first subdomain of the reporter protein and said first test peptide or protein;
- fusing an oligonucleotide or a gene encoding for a second test peptide or protein to the DNA sequence encoding for said complementary second subdomain of the reporter protein, thereby creating a second DNA fusion sequence encoding for a fusion protein comprising said complementary second subdomain of the reporter protein and said second test peptide or protein;
- (co-) expressing said fusion protein comprising said first subdomain of the reporter protein and said first test peptide or protein, and said fusion protein comprising said second complementary subdomain of the reporter protein and said second test peptide or protein in a suitable prokaryotic or eukaryotic host cell;

- screening and/or selecting for interruption of interaction of said first subdomain and said second subdomain under the influence of one or more test agents.

30. (previously presented) A process for the identification of fragmentation sites in a reporter protein for use in a two-hybrid system, comprising a step of random circular permutation of a gene and/or the expressed polypeptide derived thereof.

31. (previously presented) A process for the generation of a recombinant DNA molecule that secures for expression of both a polypeptide product comprising a first subdomain of a reporter protein and a complementary second subdomain of a reporter protein from said recombinant DNA molecule, comprising a step of transforming a host cell line that allows for homologous recombination of DNA.